## **SEQUENCE LISTING**

<110> Novozymes A/S
Svendsen, Allan
Andersen, Carsten
Borchert, Torben Vedel

<120> Pullulanase variants and methods for preparing such variants with
predetermined properties

<130> 6072.204-US

<140> To Be Assigned

<141> 2001-08-21

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<170> PatentIn version 3.1

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70

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gat Asp	cgg Arg	att Ile 755	aaa Lys	atg Met	gat Asp	gaa Glu	ctc Leu 760	gca Ala	caa Gln	gca Ala	gtt Val	gtt Val 765	atg Met	acc Thr	tca Ser	2304
caa Gln	ggc Gly 770	gtt Val	cca Pro	ttc Phe	atg Met	caa Gln 775	ggc Gly	ggg Gly	gaa Glu	gaa Glu	atg Met 780	ctt Leu	cgt Arg	aca Thr	aaa Lys	2352
ggc Gly 785	ĠТу	aac Asn	gac Asp	aat Asn	agt Ser 790	Tyr	aat Asn	gca Ala	ggc Gly	gat Asp 795	Ala	gtc Val	aat Asn	gag Glu	ttt Phe 800	2400
gat Asp	tgg Trp	agc Ser	agg Arg	aaa Lys 805	Āla	caa Gln	tat Tyr	cca Pro	gat Asp 810	٧a٦	ttc Phe	aac Asn	tat Tyr	tat Tyr 815	agc Ser	2448
999 G1y	cta Leu	atc Ile	cac His 820	Leu	cgt Arg	ctt Leu	gat Asp	cac His 825	Pro	gcc Ala	ttc Phe	cgc Arg	atg Met 830	Thr	aca Thr	2496
gct Ala	aat Asn	gaa Glu 835	ılle	aat Asn	agc Ser	cac His	ctc Leu 840	Gln	ttc Phe	cta Leu	aat Asn	agt Ser 845	Pro	gag Glu	aac Asn	2544

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aat Asn 865	atc Ile	att Ile	gtt val	gtt val	tat Tyr 870	aac Asn	cca Pro	aat Asn	aaa Lys	act Thr 875	gta Val	gca Ala	acc Thr	atc Ile	aat Asn 880	2640
ttg Leu	ccg Pro	agc Ser	ggg Gly	aaa Lys 885	tgg Trp	gca Ala	atc Ile	aat Asn	gct Ala 890	acg Thr	agc Ser	ggt Gly	aag Lys	gta Val 895	gga Gly	2688
gaa Glu	tcc Ser	acc Thr	ctt Leu 900	ggt Gly	caa Gln	gca Ala	gag Glu	gga Gly 905	agt Ser	gtc Val	caa Gln	gta Val	cca Pro 910	ggt Gly	ata Ile	2736
tct Ser	atg Met	atg Met 915	atc Ile	ctt Leu	cat His	caa Gln	gag Glu 920	gta Val	agc Ser	cca Pro	gac Asp	cac His 925	ggt Gly	aaa Lys	aag Lys	2784
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<212> **PRT** 

<213> Bacillus deramificans

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Ala Glu Tyr Asp Phe Asn Gln Pro Ala Asp Ser Phe Gly Ala Val Ala 35 40 45

Ser Ala Asp Ile Pro Gly Asn Pro Ser Gln Val Gly Ile Ile Val Arg 50 55 60

Thr Gln Asp Trp Thr Lys Asp Val Ser Ala Asp Arg Tyr Ile Asp Leu 65 70 75 80

Ser Lys Gly Asn Glu Val Trp Leu Val Glu Gly Asn Ser Gln Ile Phe  $85 \hspace{1cm} 90 \hspace{1cm} 95$ 

Tyr Asn Glu Lys Asp Ala Glu Asp Ala Ala Lys Pro Ala Val Ser Asn 100 105 110

Ala Tyr Leu Asp Ala Ser Asn Gln Val Leu Val Lys Leu Ser Gln Pro

Leu Thr Leu Gly Glu Gly Ala Ser Gly Phe Thr Val His Asp Asp Thr 130 140 Ala Asn Lys Asp Ile Pro Val Thr Ser Val Lys Asp Ala Ser Leu Gly
145 150 155 160 Gln Asp Val Thr Ala Val Leu Ala Gly Thr Phe Gln His Ile Phe Gly 165 170 175 Gly Ser Asp Trp Ala Pro Asp Asn His Ser Thr Leu Leu Lys Lys Val 180 185 190 Thr Asn Asn Leu Tyr Gln Phe Ser Gly Asp Leu Pro Glu Gly Asn Tyr 195 200 205 Gln Tyr Lys Val Ala Leu Asn Asp Ser Trp Asn Asn Pro Ser Tyr Pro 210 215 220 Ser Asp Asn Ile Asn Leu Thr Val Pro Ala Gly Gly Ala His Val Thr 225 230 235 240 Phe Ser Tyr Ile Pro Ser Thr His Ala Val Tyr Asp Thr Ile Asn Asn 245 250 255 Pro Asn Ala Asp Leu Gln Val Glu Ser Gly Val Lys Thr Asp Leu Val 260 270 Thr Val Thr Leu Gly Glu Asp Pro Asp Val Ser His Thr Leu Ser Ile 275 280 285 Gln Thr Asp Gly Tyr Gln Ala Lys Gln Val Ile Pro Arg Asn Val Leu 290 295 300 Asn Ser Ser Gln Tyr Tyr Tyr Ser Gly Asp Asp Leu Gly Asn Thr Tyr 305 310 315 320Thr Gln Lys Ala Thr Thr Phe Lys Val Trp Ala Pro Thr Ser Thr Gln
325 330 335 Val Asn Val Leu Leu Tyr Asp Ser Ala Thr Gly Ser Val Thr Lys Ile 340 345 350 Val Pro Met Thr Ala Ser Gly His Gly Val Trp Glu Ala Thr Val Asn 355 360 365 Gln Asn Leu Glu Asn Trp Tyr Tyr Met Tyr Glu Val Thr Gly Gln Gly

Ser Thr Arg Thr Ala Val Asp Pro Tyr Ala Thr Ala Ile Ala Pro Asn 385 390 395 400 Gly Thr Arg Gly Met Ile Val Asp Leu Ala Lys Thr Asp Pro Ala Gly
405 410 415 Trp Asn Ser Asp Lys His Ile Thr Pro Lys Asn Ile Glu Asp Glu Val 420 425 430 Ile Tyr Glu Met Asp Val Arg Asp Phe Ser Ile Asp Pro Asn Ser Gly 435 440 445 Met Lys Asn Lys Gly Lys Tyr Leu Ala Leu Thr Glu Lys Gly Thr Lys 450 460 Gly Pro Asp Asn Val Lys Thr Gly Ile Asp Ser Leu Lys Gln Leu Gly 465 470 475 Ile Thr His Val Gln Leu Met Pro Val Phe Ala Ser Asn Ser Val Asp 485 490 495 Glu Thr Asp Pro Thr Gln Asp Asn Trp Gly Tyr Asp Pro Arg Asn Tyr 500 505 510 Asp Val Pro Glu Gly Gln Tyr Ala Thr Asn Ala Asn Gly Asn Ala Arg 515 520 525 Ile Lys Glu Phe Lys Glu Met Val Leu Ser Leu His Arg Glu His Ile 530 535 540 Gly Val Asn Met Asp Val Val Tyr Asn His Thr Phe Ala Thr Gln Ile 545 550 555 560 Ser Asp Phe Asp Lys Ile Val Pro Glu Tyr Tyr Tyr Arg Thr Asp Asp 565 570 575 Ala Gly Asn Tyr Thr Asn Gly Ser Gly Thr Gly Asn Glu Ile Ala Ala 580 585 590 Glu Arg Pro Met Val Gln Lys Phe Ile Ile Asp Ser Leu Lys Tyr Trp 595 600 605 Val Asn Glu Tyr His Ile Asp Gly Phe Arg Phe Asp Leu Met Ala Leu 610 620

Leu Gly Lys Asp Thr Met Ser Lys Ala Ala Ser Glu Leu His Ala Ile

Asn Pro Gly Ile Ala Leu Tyr Gly Glu Pro Trp Thr Gly Gly Thr Ser 645 650 655 Ala Leu Pro Asp Asp Gln Leu Leu Thr Lys Gly Ala Gln Lys Gly Met 660 665 670 Gly Val Ala Val Phe Asn Asp Asn Leu Arg Asn Ala Leu Asp Gly Asn 675 680 685 Phe Asp Ser Ser Ala Gln Gly Phe Ala Thr Gly Ala Thr Gly Leu 690 700 Thr Asp Ala Ile Lys Asn Gly Val Glu Gly Ser Ile Asn Asp Phe Thr 705 710 715 720 Ser Ser Pro Gly Glu Thr Ile Asn Tyr Val Thr Ser His Asp Asn Tyr 725 730 735 Thr Leu Trp Asp Lys Ile Ala Leu Ser Asn Pro Asn Asp Ser Glu Ala 740 745 750 Asp Arg Ile Lys Met Asp Glu Leu Ala Gln Ala Val Val Met Thr Ser 755 760 765 Gln Gly Val Pro Phe Met Gln Gly Gly Glu Glu Met Leu Arg Thr Lys 770 775 780 Gly Gly Asn Asp Asn Ser Tyr Asn Ala Gly Asp Ala Val Asn Glu Phe 785 790 795 800 Asp Trp Ser Arg Lys Ala Gln Tyr Pro Asp Val Phe Asn Tyr Tyr Ser 805 810 815 Gly Leu Ile His Leu Arg Leu Asp His Pro Ala Phe Arg Met Thr Thr 820 825 830 Ala Asn Glu Ile Asn Ser His Leu Gln Phe Leu Asn Ser Pro Glu Asn 835 840 845 Thr Val Ala Tyr Glu Leu Thr Asp His Val Asn Lys Asp Lys Trp Gly 850 860 Asn Ile Ile Val Val Tyr Asn Pro Asn Lys Thr Val Ala Thr Ile Asn 865 870 875 880 Leu Pro Ser Gly Lys Trp Ala Ile Asn Ala Thr Ser Gly Lys Val Gly

16

885 890 895

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Ser Met Met Ile Leu His Gln Glu Val Ser Pro Asp His Gly Lys Lys 915 920 925

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<212> DNA

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ggt Gly	aat Asn	gga G1y 35	gca Ala	gca Ala	tac Tyr	gag Glu	ttt Phe 40	tct Ser	gga Gly	aag Lys	gat Asp	gat Asp 45	ttt Phe	ggc Gly	gtt Val	1	.44
aaa Lys	gca Ala 50	gat Asp	gtt val	caa Gln	gtg Val	cct Pro 55	ggg Gly	gat Asp	gat Asp	aca Thr	cag Gln 60	gta Val	ggt Gly	ctg Leu	att Ile	1	.92
gtc val 65	cgt Arg	aca Thr	aat Asn	gat Asp	tgg Trp 70	agc Ser	caa Gln	aaa Lys	aat Asn	aca Thr 75	tca Ser	gac Asp	gat Asp	ctc Leu	cat His 80	2	240
att Ile	gat Asp	ctg Leu	aca Thr	aag Lys 85	ggg Gly	cat His	gaa Glu	ata Ile	tgg Trp 90	att Ile	gtt Val	cag Gln	ggg Gly	gat Asp 95	ccc Pro	2	288
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gtt Val	tcg Ser	aat Asn 115	gcg Ala	tat Tyr	ttg Leu	gat Asp	aat Asn 120	gaa Glu	aaa Lys	aca Thr	gta Val	ttg Leu 125	gca Ala	aag Lys	cta Leu	3	384

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gat Asp 145	aaa Lys	aca Thr	aca Thr	ggg Gly	gaa Glu 150	caa Gln	att Ile	cca Pro	gtt val	acc Thr 155	gct Ala	gca Ala	aca Thr	aat Asn	gcg Ala 160	480
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						gga Gly										768
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cat His	caa Gln	cag Gln	aca Thr	cct Pro 325	gcg Ala	aac Asn	cca Pro	gtg Val	gat Asp 330	gaa Glu	gta Val	atc Ile	tac Tyr	gaa Glu 335	gtg Val	1008
cat His	gtg Val	cgt Arg	gat Asp 340	ttt Phe	tcg Ser	att Ile	gat Asp	gct Ala 345	aat Asn	tca Ser	ggc Gly	atg Met	aaa Lys 350	aat Asn	aaa Lys	1056
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gtg Val	aaa Lys 370	acg Thr	ggt Gly	att Ile	gat Asp	agt Ser 375	ttg Leu	aag Lys	gaa Glu	tta Leu	gga Gly 380	atc Ile	aat Asn	gct Ala	gtt Val	1152

caa Gln 385	tta Leu	cag Gln	ccg Pro	att Ile	gaa Glu 390	gaa Glu	ttt Phe	aac Asn	agc Ser	att Ile 395	gat Asp	gaa Glu	acc Thr	caa Gln	cca Pro 400	1200
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aag Lys	caa Gln	ctg Leu 435	att Ile	caa Gln	agc Ser	att Ile	cat His 440	aaa Lys	gat Asp	cgg Arg	att Ile	gct Ala 445	atc Ile	aat Asn	atg Met	1344
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					aaa Lys											1728
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					gga Gly											1872
gaa Glu 625	acc Thr	att Ile	aac Asn	tat Tyr	gta Val 630	aca Thr	agc Ser	cat His	gat Asp	aat Asn 635	atg Met	aca Thr	ttg Leu	tgg Trp	gat Asp 640	1920

aaa att ago Lys Ile Ser	gca agt aat Ala Ser Asi 645	ccg aac Pro Asn	gat aca Asp Thr 650	caa gca Gln Ala	gat cga Asp Arg	att aag Ile Lys 655	1968
atg gat gaa Met Asp Glu	ttg gct caa Leu Ala Glr 660	a gct gtg n Ala Val	gta ttt Val Phe 665	act tca Thr Ser	caa ggg Gln Gly 670	gta cca Val Pro	2016
ttt atg caa Phe Met Gln 675	ggt gga gaa Gly Gly Glu	gaa atg Glu Met 680	ctg cgg Leu Arg	aca aaa Thr Lys	ggc ggt Gly Gly 685	aat gat Asn Asp	2064
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aaa gca caa Lys Ala Gln 705	ttt gaa aat Phe Glu Asr 710	val Phe	gac tac Asp Tyr	tat tct Tyr Ser 715	tgg ttg Trp Leu	att cat Ile His 720	2160
cta cgt gat Leu Arg Asp	aat cac cca Asn His Pro 725	gca ttc Ala Phe	cgt atg Arg Met 730	acg aca Thr Thr	gcg gat Ala Asp	caa atc Gln Ile 735	2208
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gaa tta aaa Glu Leu Lys 755	aat cat gco Asn His Ala	aat cat Asn His 760	gat aaa Asp Lys	tgg aaa Trp Lys	aac att Asn Ile 765	ata gtt Ile Val	2304
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ggc cat gta Gly His Val	aat ggc acc Asn Gly Thr 805	gtt gag Val Glu	gtg cca Val Pro 810	gct ctt Ala Leu	agt acg Ser Thr	atc att Ile Ile 815	2448
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<211> 829

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Thr Met Ala Lys Ile Ser Lys Glu Leu His Ala Ile Asn Pro Gly Ile 530 540 Val Leu Tyr Gly Glu Pro Trp Thr Gly Gly Thr Ser Gly Leu Ser Ser 545 550 555 560 Asp Gln Leu Val Thr Lys Gly Gln Gln Lys Gly Leu Gly Ile Gly Val 565 570 575 Phe Asn Asp Asn Ile Arg Asn Gly Leu Asp Gly Asn Val Phe Asp Lys 580 585 590 Ser Ala Gln Gly Phe Ala Thr Gly Asp Pro Asn Gln Val Asn Val Ile 595 600 605 Lys Asn Arg Val Met Gly Ser Ile Ser Asp Phe Thr Ser Ala Pro Ser 610 620 Glu Thr Ile Asn Tyr Val Thr Ser His Asp Asn Met Thr Leu Trp Asp 625 630 635 640 Lys Ile Ser Ala Ser Asn Pro Asn Asp Thr Gln Ala Asp Arg Ile Lys
645 650 655 Met Asp Glu Leu Ala Gln Ala Val Val Phe Thr Ser Gln Gly Val Pro 660 665 670 Phe Met Gln Gly Glu Glu Met Leu Arg Thr Lys Gly Gly Asn Asp 675 680 685 Asn Ser Tyr Asn Ala Gly Asp Ser Val Asn Gln Phe Asp Trp Ser Arg 690 695 700 Lys Ala Gln Phe Glu Asn Val Phe Asp Tyr Tyr Ser Trp Leu Ile His 705 710 715 720 Leu Arg Asp Asn His Pro Ala Phe Arg Met Thr Thr Ala Asp Gln Ile 725 730 735 Lys Gln Asn Leu Thr Phe Leu Asp Ser Pro Thr Asn Thr Val Ala Phe 740 745 750 Glu Leu Lys Asn His Ala Asn His Asp Lys Trp Lys Asn Ile Ile Val 755 760 765 Met Tyr Asn Pro Asn Lys Thr Ala Gln Thr Leu Thr Leu Pro Ser Gly 770 780 Asn Trp Thr Ile Val Gly Leu Gly Asn Gln Val Gly Glu Lys Ser Leu 785 790 795 800 Gly His Val Asn Gly Thr Val Glu Val Pro Ala Leu Ser Thr Ile Ile 805 810 815 Leu His Gln Gly Thr Ser Glu Asp Val Ile Asp Gln Asn 820 825 <210> 7 <211> 23 <212> DNA <213> Artificial Sequence <220> <223> Primer 132011 <400> 7 cgcttcggaa tcattaggat tgc 23 <210> 8 <211> 27 <212> DNA <213> Artificial Sequence <220> <223> Primer 132012 <400> 8 27 gcttccgttt tgccttaatg gcgctgc <210> 9 <211> 23 <212> DNA <213> Artificial Sequence <220>

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